



SEQ LIST US provisional App. No. 60051917

SEQUENCE LISTING

SEQ ID NO: 1
SEQUENCE LENGTH: 21
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
SEQUENCE DESCRIPTION:
CTC TAG CAT GCG AAA ATC TAG

SEQ ID NO: 2
SEQUENCE LENGTH: 20
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
SEQUENCE DESCRIPTION:
CTG CAG GCC TGC AAG CTT GG

SEQ ID NO: 3
SEQUENCE LENGTH: 23
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
SEQUENCE DESCRIPTION:
ATC CTT TGT ATT TGA TTA AAG

SEQ ID NO: 4
SEQUENCE LENGTH: 20
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
SEQUENCE DESCRIPTION:
TCT AGA GTC GAC CTG CAG GC

SEQ ID NO: 5
SEQUENCE LENGTH: 552
SEQUENCE TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE: *Luciola cruciata* and *Photinus pyralis*
SEQUENCE DESCRIPTION:
Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Val Gly Pro Lys
1 5 10 15
Pro Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Thr Gln Leu Arg
20 25 30
Lys Tyr Met Glu Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr
35 40 45
Asn Ala Val Thr Gly Val Asp Tyr Ser Tyr Ala Glu Tyr Leu Glu
50 55 60
Lys Ser Cys Cys Leu Gly Lys Ala Leu Gln Asn Tyr Gly Leu Val
65 70 75
Val Asp Gly Arg Ile Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe

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	80		85		90
Phe Ile Pro Val	Ile	Ala Gly Leu Phe	Ile	Gly Val Gly Val	Ala
	95		100		105
Pro Thr Asn Glu	Ile	Tyr Thr Leu Arg	Glu	Leu Val His Ser	Leu
	110		115		120
Gly Ile Ser Lys	Pro	Thr Ile Val Phe	Ser	Ser Lys Lys Gly	Leu
	125		130		135
Asp Lys Val Ile	Thr	Val Gln Lys Thr	Val	Thr Thr Ile Lys	Thr
	140		145		150
Ile Val Ile Leu	Asp	Ser Lys Val Asp	Tyr	Arg Gly Tyr Gln	Cys
	155		160		165
Leu Asp Thr Phe	Ile	Lys Arg Asn Thr	Pro	Pro Gly Phe Gln	Ala
	170		175		180
Ser Ser Phe Lys	Thr	Val Glu Val Asp	Arg	Lys Glu Gln Val	Ala
	185		190		195
Leu Ile Met Asn	Ser	Ser Gly Ser Thr	Gly	Leu Pro Lys Gly	Val
	200		205		210
Gln Leu Thr His	Glu	Asn Thr Val Thr	Arg	Phe Ser His Ala	Arg
	215		220		225
Asp Pro Ile Phe	Gly	Asn Gln Ile Ile	Pro	Asp Thr Ala Ile	Leu
	230		235		240
Ser Val Val Pro	Phe	His His Gly Phe	Gly	Met Phe Thr Thr	Leu
	245		250		255
Gly Tyr Leu Ile	Cys	Gly Phe Arg Val	Val	Leu Met Tyr Arg	Phe
	260		265		270
Glu Glu Glu Leu	Phe	Leu Arg Ser Leu	Gln	Asp Tyr Lys Ile	Gln
	275		280		285
Ser Ala Leu Leu	Val	Pro Thr Leu Phe	Ser	Phe Phe Ala Lys	Ser
	290		295		300
Thr Leu Ile Asp	Lys	Tyr Asp Leu Ser	Asn	Leu His Glu Ile	Ala
	305		310		315
Ser Gly Gly Ala	Pro	Leu Ser Lys Glu	Val	Gly Glu Ala Val	Ala
	320		325		330
Lys Arg Phe His	Leu	Pro Gly Ile Arg	Gln	Gly Tyr Gly Leu	Thr
	335		340		345
Glu Thr Thr Ser	Ala	Ile Leu Ile Thr	Pro	Glu Gly Asp Asp	Lys
	350		355		360
Pro Gly Ala Val	Gly	Lys Val Val Pro	Phe	Phe Glu Ala Lys	Val
	365		370		375
Val Asp Leu Asp	Thr	Gly Lys Thr Leu	Gly	Val Asn Gln Arg	Gly
	380		385		390
Glu Leu Cys Val	Arg	Gly Pro Met Ile	Met	Ser Gly Tyr Val	Asn
	395		400		405
Asn Pro Glu Ala	Thr	Asn Ala Leu Ile	Asp	Lys Asp Gly Trp	Leu
	410		415		420
His Ser Gly Asp	Ile	Ala Tyr Trp Asp	Glu	Asp Glu His Phe	Phe
	425		430		435
Ile Val Asp Arg	Leu	Lys Ser Leu Ile	Lys	Tyr Lys Gly Tyr	Gln
	440		445		450
Val Ala Pro Ala	Glu	Leu Glu Ser Ile	Leu	Leu Gln His Pro	Asn
	455		460		465
Ile Phe Asp Ala	Gly	Val Ala Gly Leu	Pro	Asp Asp Asp Ala	Gly
	470		475		480
Glu Leu Pro Ala	Ala	Val Val Val Leu	Glu	His Gly Lys Thr	Met
	485		490		495
Thr Glu Lys Glu	Ile	Val Asp Tyr Val	Ala	Ser Gln Val Thr	Thr

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500	Ala Lys Lys Leu	Arg Gly Gly Val Val	505	Phe Val Asp Glu Val	510	Pro
515	Lys Gly Leu Thr	Gly Lys Leu Asp Ala	520	Arg Lys Ile Arg Glu	525	Ile
530	Leu Ile Lys Ala	Lys Lys Gly Gly Lys	535	Ser Lys Leu	540	
545			550		552	

SEQ ID NO: 6

SEQUENCE LENGTH: 1656

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE: *Luciola cruciata* and *Photinus pyralis*

SEQUENCE DESCRIPTION:

ATG GAA AAC ATG GAA AAC GAT GAA AAT ATT GTA GTT GGA CCT AAA CCG	48
TTT TAC CCT ATC GAA GAG GGA TCT GCT GGA ACA CAA TTA CGC AAA TAC	96
ATG GAG CGA TAT GCA AAA CTT GGC GCA ATT GCT TTT ACA AAT GCA GTT	144
ACT GGT GTT GAT TAT TCT TAC GCC GAA TAC TTG GAG AAA TCA TGT TGT	192
CTA GGA AAA GCT TTG CAA AAT TAT GGT TTG GTT GTT GAT GGC AGA ATT	240
GCG TTA TGC AGT GAA AAC TGT GAA GAA TTT TTT ATT CCT GTA ATA GCC	288
GGA CTG TTT ATA GGT GTA GGT GTT GCA CCC ACT AAT GAG ATT TAC ACT	366
TTA CGT GAA CTG GTT CAC AGT TTA GGT ATC TCT AAA CCA ACA ATT GTA	384
TTT AGT TCT AAA AAA GGC TTA GAT AAA GTT ATA ACA GTA CAG AAA ACA	432
GTA ACT ACT ATT AAA ACC ATT GTT ATA CTA GAT AGC AAA GTT GAT TAT	480
CGA GGA TAT CAA TGT CTG GAC ACC TTT ATA AAA AGA AAC ACT CCA CCA	528
GGT TTT CAA GCA TCC AGT TTC AAA ACT GTG GAA GTT GAC CGT AAA GAA	576
CAA GTT GCT CTT ATA ATG AAC TCT TCG GGT TCT ACC GGT TTG CCA AAA	624
GGC GTA CAA CTT ACT CAC GAA AAT ACA GTC ACT AGA TTT TCG CAT GCC	672
AGA GAT CCT ATT TTT GGC AAT CAA ATC ATT CCG GAT ACT GCG ATT TTA	720
AGT GTT GTT CCA TTC CAT CAC GGT TTT GGA ATG TTT ACT ACA CTC GGA	768
TAT TTG ATA TGT GGA TTT CGA GTC GTC TTA ATG TAT AGA TTT GAA GAA	816
GAG CTG TTT TTA CGA TCC CTT CAG GAT TAC AAA ATT CAA AGT GCG TTG	864
CTA GTA CCA ACC CTA TTT TCA TTC TTC GCC AAA AGC ACT CTG ATT GAC	912
AAA TAC GAT TTA TCT AAT TTA CAC GAA ATT GCT TCT GGG GGC GCA CCT	960
CTT TCG AAA GAA GTC GGG GAA GCG GTT GCA AAA CGC TTC CAT CTT CCA	1008
GGG ATA CGA CAA GGA TAT GGG CTC ACT GAG ACT ACA TCA GCT ATT CTG	1056
ATT ACA CCC GAG GGG GAT GAT AAA CCG GGC GCG GTC GGT AAA GTT GTT	1104
CCA TTT TTT GAA GCG AAG GTT GTG GAT CTG GAT ACC GGG AAA ACG CTG	1152
GGC GTT AAT CAG AGA GGC GAA TTA TGT GTC AGA GGA CCT ATG ATT ATG	1200
TCC GGT TAT GTA AAC AAT CCG GAA GCG ACC AAC GCC TTG ATT GAC AAG	1248
GAT GGA TGG CTA CAT TCT GGA GAC ATA GCT TAC TGG GAC GAA GAC GAA	1296
CAC TTC TTC ATA GTT GAC CGC TTG AAG TCT TTA ATT AAA TAC AAA GGA	1344
TAT CAG GTG GCC CCC GCT GAA TTG GAA TCG ATA TTG TTA CAA CAC CCC	1392
AAC ATC TTC GAC GCG GGC GTG GCA GGT CTT CCC GAC GAT GAC GCC GGT	1440
GAA CTT CCC GCC GCC GTT GTT GTT TTG GAG CAC GGA AAG ACG ATG ACG	1488
GAA AAA GAG ATC GTG GAT TAC GTC GCC AGT CAA GTA ACA ACC GCG AAA	1536
AAG TTG CGC GGA GGA GTT GTG TTT GTG GAC GAA GTA CCG AAA GGT CTT	1584
ACC GGA AAA CTC GAC GCA AGA AAA ATC AGA GAG ATC CTC ATA AAG GCC	1632
AAG AAG GGC GGA AAG TCC AAA TTG	1656

SEQ ID NO: 7

SEQUENCE LENGTH: 552

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

SEQ LIST US provisional App. No. 60051917

MOLECULE TYPE: peptide

ORIGINAL SOURCE: *Luciola cruciata* and *Photinus pyralis*

SEQUENCE DESCRIPTION:

Met	Glu	Asn	Met	Glu	Asn	Asp	Glu	Asn	Ile	Val	Val	Gly	Pro	Lys	1	5	10	15
Pro	Phe	Tyr	Pro	Ile	Glu	Glu	Gly	Ser	Ala	Gly	Thr	Gln	Leu	Arg	20	25	30	35
Lys	Tyr	Met	Glu	Arg	Tyr	Ala	Lys	Leu	Gly	Ala	Ile	Ala	Phe	Thr	40	45	50	55
Asn	Ala	Val	Thr	Gly	Val	Asp	Tyr	Ser	Tyr	Ala	Glu	Tyr	Leu	Glu	60	65	70	75
Lys	Ser	Cys	Cys	Leu	Gly	Lys	Ala	Leu	Gln	Asn	Tyr	Gly	Leu	Val	80	85	90	95
Val	Asp	Gly	Arg	Ile	Ala	Leu	Cys	Ser	Glu	Asn	Cys	Glu	Glu	Phe	100	105	110	115
Phe	Ile	Pro	Val	Ile	Ala	Gly	Leu	Phe	Ile	Gly	Val	Gly	Val	Ala	120	125	130	135
Pro	Thr	Asn	Glu	Ile	Tyr	Thr	Leu	Arg	Glu	Leu	Val	His	Ser	Leu	140	145	150	155
Gly	Ile	Ser	Lys	Pro	Thr	Ile	Val	Phe	Ser	Ser	Lys	Lys	Gly	Leu	160	165	170	175
Asp	Lys	Val	Ile	Thr	Val	Gln	Lys	Thr	Val	Thr	Thr	Ile	Lys	Thr	180	185	190	195
Ile	Val	Ile	Leu	Asp	Ser	Lys	Val	Asp	Tyr	Arg	Gly	Tyr	Gln	Cys	200	205	210	215
Leu	Asp	Thr	Phe	Ile	Lys	Arg	Asn	Thr	Pro	Pro	Gly	Phe	Gln	Ala	220	225	230	235
Ser	Ser	Phe	Lys	Thr	Val	Glu	Val	Asp	Arg	Lys	Glu	Gln	Val	Ala	240	245	250	255
Leu	Ile	Met	Asn	Ser	Ser	Gly	Ser	Thr	Gly	Leu	Pro	Lys	Gly	Val	260	265	270	275
Gln	Leu	Thr	His	Glu	Asn	Ile	Val	Thr	Arg	Phe	Ser	His	Ala	Arg	280	285	290	295
Asp	Pro	Ile	Tyr	Gly	Asn	Gln	Val	Ser	Pro	Gly	Thr	Ala	Val	Leu	300	305	310	315
Thr	Val	Val	Pro	Phe	His	His	Gly	Phe	Gly	Met	Phe	Thr	Thr	Leu	320	325	330	335
Gly	Tyr	Leu	Ile	Cys	Gly	Phe	Arg	Val	Val	Met	Leu	Thr	Lys	Phe	340	345	350	355
Asp	Glu	Glu	Thr	Phe	Leu	Lys	Thr	Leu	Gln	Asp	Tyr	Lys	Cys	Thr	360	365	370	375
Ser	Val	Ile	Leu	Val	Pro	Thr	Leu	Phe	Ala	Ile	Leu	Asn	Lys	Ser	380	385	390	395
Glu	Leu	Leu	Asn	Lys	Tyr	Asp	Leu	Ser	Asn	Leu	Val	Glu	Ile	Ala	400	405	410	415
Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys	Glu	Val	Gly	Glu	Ala	Val	Ala	420	425	430	435
Arg	Arg	Phe	Asn	Leu	Pro	Gly	Val	Arg	Gln	Gly	Tyr	Gly	Leu	Thr	440	445	450	455
Glu	Thr	Thr	Ser	Ala	Ile	Ile	Ile	Thr	Pro	Glu	Gly	Asp	Asp	Lys	460	465	470	475
Pro	Gly	Ala	Ser	Gly	Lys	Val	Val	Pro	Leu	Phe	Lys	Ala	Lys	Val	480	485	490	495
Ile	Asp	Leu	Asp	Thr	Lys	Lys	Ser	Leu	Gly	Pro	Asn	Arg	Arg	Gly	500	505	510	515
Glu	Val	Cys	Val	Lys	Gly	Pro	Met	Leu	Met	Lys	Gly	Tyr	Val	Asn	520	525	530	535

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Asn Pro Glu Ala Thr	395	Lys Glu Leu Ile	400	Asp Glu Glu Gly Trp	405
His Thr Gly Asp Ile	410	Gly Tyr Tyr Asp	415	Glu Glu Lys His Phe	420
Ile Val Asp Arg Leu	425	Lys Ser Leu Ile	430	Lys Tyr Lys Gly Tyr	435
Val Ala Pro Ala Glu	440	Leu Glu Ser Ile	445	Leu Leu Gln His Pro	450
Ile Phe Asp Ala Gly	455	Val Ala Gly Leu	460	Pro Asp Asp Asp Ala	465
Glu Leu Pro Ala Ala	470	Val Val Val Leu	475	Glu His Gly Lys Thr	480
Thr Glu Lys Glu Ile	485	Val Asp Tyr Val	490	Ala Ser Gln Val Thr	495
Ala Lys Lys Leu Arg	500	Gly Gly Val Val	505	Phe Val Asp Glu Val	510
Lys Gly Leu Thr Gly	515	Lys Leu Asp Ala	520	Arg Lys Ile Arg Glu	525
Leu Ile Lys Ala Lys	530	Lys Gly Gly Lys	535	Ser Lys Leu	540
	545		550		552

SEQ ID NO: 8

SEQUENCE LENGTH: 1656

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE: *Luciola cruciata* and *Photinus pyralis*

SEQUENCE DESCRIPTION:

ATG GAA AAC ATG GAA AAC GAT GAA AAT ATT GTA GTT GGA CCT AAA CCG	48
TTT TAC CCT ATC GAA GAG GGA TCT GCT GGA ACA CAA TTA CGC AAA TAC	96
ATG GAG CGA TAT GCA AAA CTT GGC GCA ATT GCT TTT ACA AAT GCA GTT	144
ACT GGT GTT GAT TAT TCT TAC GCC GAA TAC TTG GAG AAA TCA TGT TGT	192
CTA GGA AAA GCT TTG CAA AAT TAT GGT TTG GTT GTT GAT GGC AGA ATT	240
GCG TTA TGC AGT GAA AAC TGT GAA GAA TTT TTT ATT CCT GTA ATA GCC	288
GGA CTG TTT ATA GGT GTA GGT GTT GCA CCC ACT AAT GAG ATT TAC ACT	336
TTA CGT GAA CTG GTT CAC AGT TTA GGT ATC TCT AAA CCA ACA ATT GTA	384
TTT AGT TCT AAA AAA GGC TTA GAT AAA GTT ATA ACA GTA CAG AAA ACA	432
GTA ACT ACT ATT AAA ACC ATT GTT ATA CTA GAT AGC AAA GTT GAT TAT	480
CGA GGA TAT CAA TGT CTG GAC ACC TTT ATA AAA AGA AAC ACT CCA CCA	528
GGT TTT CAA GCA TCC AGT TTC AAA ACT GTG GAA GTT GAC CGT AAA GAA	576
CAA GTT GCT CTT ATA ATG AAC TCT TCG GGT TCT ACC GGT TTG CCA AAA	624
GGC GTA CAA CTT ACT CAC GAA AAT ATA GTC ACT AGA TTT TCT CAT GCT	672
AGA GAT CCG ATT TAT GGT AAC CAA GTT TCA CCA GGC ACC GCT GTT TTA	720
ACT GTC GTT CCA TTC CAT CAT GGT TTT GGT ATG TTC ACT ACT CTA GGG	768
TAT TTA ATT TGT GGT TTT CGT GTT GTA ATG TTA ACA AAA TTC GAT GAA	816
GAA ACA TTT TTA AAA ACT CTA CAA GAT TAT AAA TGT ACA AGT GTT ATT	864
CTT GTA CCG ACC TTG TTT GCA ATT CTC AAC AAA AGT GAA TTA CTC AAT	912
AAA TAC GAT TTG TCA AAT TTA GTT GAG ATT GCA TCT GGC GGA GCA CCT	960
TTA TCA AAA GAA GTT GGT GAA GCT GTT GCT AGA CGC TTT AAT CTT CCC	1008
GGT GTT CGT CAA GGT TAT GGT TTA ACA GAA ACA ACA TCT GCC ATT ATT	1056
ATT ACA CCG GAA GGT GAC GAT AAA CCA GGA GCT TCT GGA AAA GTC GTG	1104
CCG TTG TTT AAA GCA AAA GTT ATT GAT CTT GAT ACT AAA AAA TCT TTA	1152
GGT CCT AAC AGA CGT GGA GAA GTT TGT GTT AAA GGA CCT ATG CTT ATG	1200
AAA GGT TAT GTA AAT AAT CCA GAA GCA ACA AAA GAA CTT ATT GAC GAA	1248

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GAA	GGT	TGG	CTG	CAC	ACC	GGA	GAT	ATT	GGA	TAT	TAT	GAT	GAA	GAA	AAA	1296
CAT	TTC	TTT	ATT	GTC	GAT	CGT	TTG	AAG	TCT	TTA	ATC	AAA	TAC	AAA	GGA	1344
TAT	CAG	GTG	GCC	CCC	GCT	GAA	TTG	GAA	TCG	ATA	TTG	TTA	CAA	CAC	CCC	1392
AAC	ATC	TTC	GAC	GCG	GGC	GTG	GCA	GGT	CTT	CCC	GAC	GAT	GAC	GCC	GGT	1440
GAA	CTT	CCC	GCC	GCC	GTT	GTT	GTT	TTG	GAG	CAC	GGA	AAG	ACG	ATG	ACG	1488
GAA	AAA	GAG	ATC	GTG	GAT	TAC	GTC	GCC	AGT	CAA	GTA	ACA	ACC	GCG	AAA	1536
AAG	TTG	CGC	GGA	GGA	GTT	GTG	TTT	GTG	GAC	GAA	GTA	CCG	AAA	GGT	CTT	1584
ACC	GGA	AAA	CTC	GAC	GCA	AGA	AAA	ATC	AGA	GAG	ATC	CTC	ATA	AAG	GCC	1632
AAG	AAG	GGC	GGA	AAG	TCC	AAA	TTG									1656